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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=4; hr=7; min=24; sec=12; ms=815;]

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Application No: 09540245 Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-02 10:18:59.302
Finished: 2008-12-02 10:19:02.950
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 648 ms
Total Warnings: 14
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

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W 402	Undefined organism found in <213> in SEQ ID (3)
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W 402	Undefined organism found in <213> in SEQ ID (5)
E 341	'Xaa' position not defined SEQID (5) POS (153)
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W 402	Undefined organism found in <213> in SEQ ID (19)
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<110> APPLICANT: Goodman, Corey
 Kid, Thomas
 Brose, Katja
 Tessier-Lavigne, Marc
 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
 <130> FILE REFERENCE: B98-031-3

<140> CURRENT APPLICATION NUMBER:09540245
 <141> CURRENT FILING DATE:2000-03-31
 <150> PRIOR APPLICATION NUMBER: 60/065,544
 <151> PRIOR FILING DATE: 1997-11-14
 <150> PRIOR APPLICATION NUMBER: 60/081,057
 <151> PRIOR FILING DATE: 1998-04-07
 <160> NUMBER OF SEQ ID NOS: 20
 <170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO 1
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 <212> TYPE: DNA
 <213> ORGANISM: human
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(4575)

<400> SEQUENCE: 1

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ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc	96
Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys	
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Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser	
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gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga	192
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly	
50 55 60	
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Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His	
65 70 75 80	
cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga	288
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg	
85 90 95	
gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga	336
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg	
100 105 110	
aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag	384
Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys	
115 120 125	
cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg	432
Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg	
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Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr	
145 150 155 160	
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165 170 175	

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Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser	
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Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu	
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Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro	
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Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser	
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Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro	
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Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn	
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gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac	1200
Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His	
385 390 395 400	
aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc	1248
Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala	
405 410 415	
aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc	1296
Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala	
420 425 430	
cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat	1344
Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr	
435 440 445	
ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc	1392
Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro	
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Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro	
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Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu	
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565 570 575	
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Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn	
580 585 590	
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Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met	
595 600 605	
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Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn	
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Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys	
725 730 735	
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Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val	
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Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala	
865 870 875 880	
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Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn	
945 950 955 960	
cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat	2928
Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp	
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Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu	
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Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr	
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